Amendments to the Claims:

The following listing of claims replaces all prior versions of the claims:

Listing of Claims:

- 1. (previously presented) A method of identifying one or more positions in a <u>protein</u> polymer family, the method comprising:
 - (a) accessing data representing a multiple sequence alignment (MSA) of a plurality of protein polymer sequences; and
 - (b) identifying one or more evolutionarily conserved amino acid positions within the MSA using the following equation:

$$\Delta G_i^{stat} = kT^* \sqrt{\sum_{x} \left(\ln \frac{P_i^x}{P_{MSA}^x} \right)^2}$$

wherein:

i is a position in the MSA;

 ΔG_i^{stat} is the conservation energy value for position i;

 P_i^x is the probability of <u>amino acid</u> monomer x at position i;

 P_{MSA}^{x} is the probability of <u>amino acid</u> monomer x in the MSA; and

kT* is an energy unit, where k is Boltzmann's constant.

- 2. (original) The method of claim 1, wherein the method is executed using a machine.
- 3. (previously presented) A program storage device comprising machine readable instructions for performing the operations recited in claim 1.
- 4. (previously presented) The method of claim 1, further comprising generating a graphical image of one or more conservation energy values calculated using the equation.
- 5-6. (canceled)

- 7. (previously presented) The method of claim 1, wherein the data accessed comprises data from the PSD-95 (Postsynaptic density protein of Mr 95kDa), Dlg (Drosophila Discs-Large protein) and ZO-1 (Zonula occludens protein 1) protein family.
- 8. (previously presented) The method of claim 1, wherein the data accessed comprises data from the p21^{ras} protein family.
- 9. (previously presented) The method of claim 1, wherein the data accessed comprises data from the hemoglobin protein family.
- 10. (currently amended) A method of identifying one or more positions in a <u>protein polymer</u> family, the method comprising:
 - (a) accessing data representing a multiple sequence alignment (MSA) of a plurality of protein polymer sequences;
 - (b) calculating a conservation energy value for each position in the MSA using the following equation:

$$\Delta G_i^{stat} = kT^* \sqrt{\sum_{x} \left(\ln \frac{P_i^x}{P_{MSA}^x} \right)^2}$$

wherein:

i is a position in the MSA;

 ΔG_i^{stat} is the conservation energy value for position i;

 P_i^x is the probability of <u>amino acid</u> monomer x at position i;

 P_{MSA}^{x} is the probability of <u>amino acid</u> monomer x in the MSA;

kT* is an energy unit, where k is Boltzmann's constant; and

- (c) identifying one or more positions within the MSA that have statistically significant conservation energy values.
- 11. (original) The method of claim 10, wherein the method is executed using a machine.

- 12. (previously presented) A program storage device comprising machine readable instructions for performing the operations recited in claim 10.
- 13. (original) The method of claim 10, further comprising generating a graphical image of the conservation energy values.

14-15. (canceled)

- 16. (previously presented) The method of claim 10, wherein the data accessed comprises data from the PSD-95 (Postsynaptic density protein of Mr 95kDa), Dlg (Drosophila Discs-Large protein) and ZO-1 (Zonula occludens protein 1) protein family.
- 17. (previously presented) The method of claim 10, wherein the data accessed comprises data from the p21^{ras} protein family.
- 18. (previously presented) The method of claim 10, wherein the data accessed comprises data from the hemoglobin protein family.

19-35. (canceled)